

Fasting inhibits aerobic glycolysis and proliferation in colorectal cancer via the Fdft1-mediated AKT/mTOR/HIF1 α pathway suppression

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Evidence suggests that fasting exerts extensive antitumor effects in various cancers, including colorectal cancer (CRC). However, the mechanism behind this response is unclear. We investigate the effect of fasting on glucose metabolism and malignancy in CRC. We find that fasting upregulates the expression of a cholesterologenic gene, Farnesyl-Diphosphate Farnesyltransferase 1 (FDFT1), during the inhibition of CRC cell aerobic glycolysis and proliferation. In addition, the downregulation of FDFT1 is correlated with malignant progression and poor prognosis in CRC. Moreover, FDFT1 acts as a critical tumor suppressor in CRC. Mechanistically, FDFT1 performs its tumor-inhibitory function by negatively regulating AKT/mTOR/HIF1 α signaling. Furthermore, mTOR inhibitor can synergize with fasting in inhibiting the proliferation of CRC. These results indicate that FDFT1 is a key downstream target of the fasting response and may be involved in CRC cell glucose metabolism. Our results suggest therapeutic implications in CRC and potential crosstalk between a cholesterologenic gene and glycolysis.

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Colorectal cancer (CRC) is one of the deadliest diseases globally, ranking third in cancer morbidity and second in cancer mortality worldwide¹. The incidence has stabilized or is declining in the US and some other developed countries, but the incidence and mortality are increasing in some developing countries, especially China and Spain^{2,3}. Although great progress has been achieved in surgical techniques and treatment for CRC, the 5-year relative survival rate of CRC patients has not changed significantly in the past decades^{4,5}. Therefore, there is an urgent need to better understand the molecular mechanisms that govern the oncogenesis and progression of CRC.

Fasting, defined as consuming no or minimal amounts of food, usually from 12 h to 3 weeks, is known for extending the lifespan in numerous experimental organisms^{6–8}. Many prospective clinical trials have shown that fasting can reduce risk factors for aging-related diseases, including cardiovascular disease, diabetes, and cancer^{9–11}. Fasting can also increase resistance to various oxidative stresses, such as acute surgical stress^{12–14}. On the molecular level, fasting is not well understood but based on the data from studies on fasting-mediated longevity and stress resistance, it is thought to work at least in part through the inhibition of insulin/*IGF-1*/*mTORC1* signaling^{15–18}. Although fasting exerts extensive antitumor effects in numerous contexts, the impact of fasting on metabolic changes in CRC remains poorly studied.

Aberrant metabolism has been considered a hallmark of cancer cells, and this important research field has recently attracted interest^{19,20}. Unlike normal cells, which derive most of their energy from mitochondrial oxidative phosphorylation, cancer cells rely on aerobic glycolysis as their primary energy resource. This process is recognized as the “Warburg effect”^{21–23}. *AKT/mTOR/HIF1 α* signaling has been suggested to play critical roles in promoting glycolysis and lactate production and thus in the “metabolic reprogramming” of cancer cells^{24–28}. However, fasting could reprogram metabolic derangements to inhibit cancer growth^{8,29–31}. Therefore, an understanding of the effects of fasting on metabolic alterations in CRC could lead to better therapeutic approaches.

Farnesyl-diphosphate farnesyltransferase 1 (*FDFT1*) encodes a membrane-associated enzyme acting at a branch point in the mevalonate pathway. The encoded protein is the first enzyme in cholesterol biosynthesis and catalyzes the dimerization of two molecules of farnesyl diphosphate via a two-step reaction to form squalene³², which plays an important role in cholesterol biosynthesis^{33,34}. Although increased *FDFT1* transcription is associated with increased invasion in prostate cancer, the exact role of *FDFT1* in CRC progression has not been investigated³⁵. However, our results indicated that fasting upregulated the expression of *FDFT1* during the inhibition of CRC cell glucose metabolism and proliferation. Clinically, high *FDFT1* expression in CRC is associated with better prognosis in The Cancer Genome Atlas (TCGA) data sets. This finding prompted us to speculate that *FDFT1* may play a negative regulatory role in glucose metabolism, which is a critical aspect in the fasting-mediated suppression of CRC oncogenesis and progression.

In this study, we provide ample evidence that fasting negatively regulates glucose metabolism and proliferation via the *FDFT1/AKT-mTOR-HIF1 α* axis in CRC. Overall, our results indicate that *FDFT1* is a key downstream target of the fasting response and involve in CRC cell glucose metabolism. More broadly, our present study also suggests potential therapeutic implications (involving fasting and *mTOR*) for CRC and implies potential crosstalk between a cholesterologenic gene and glycolysis.

Results

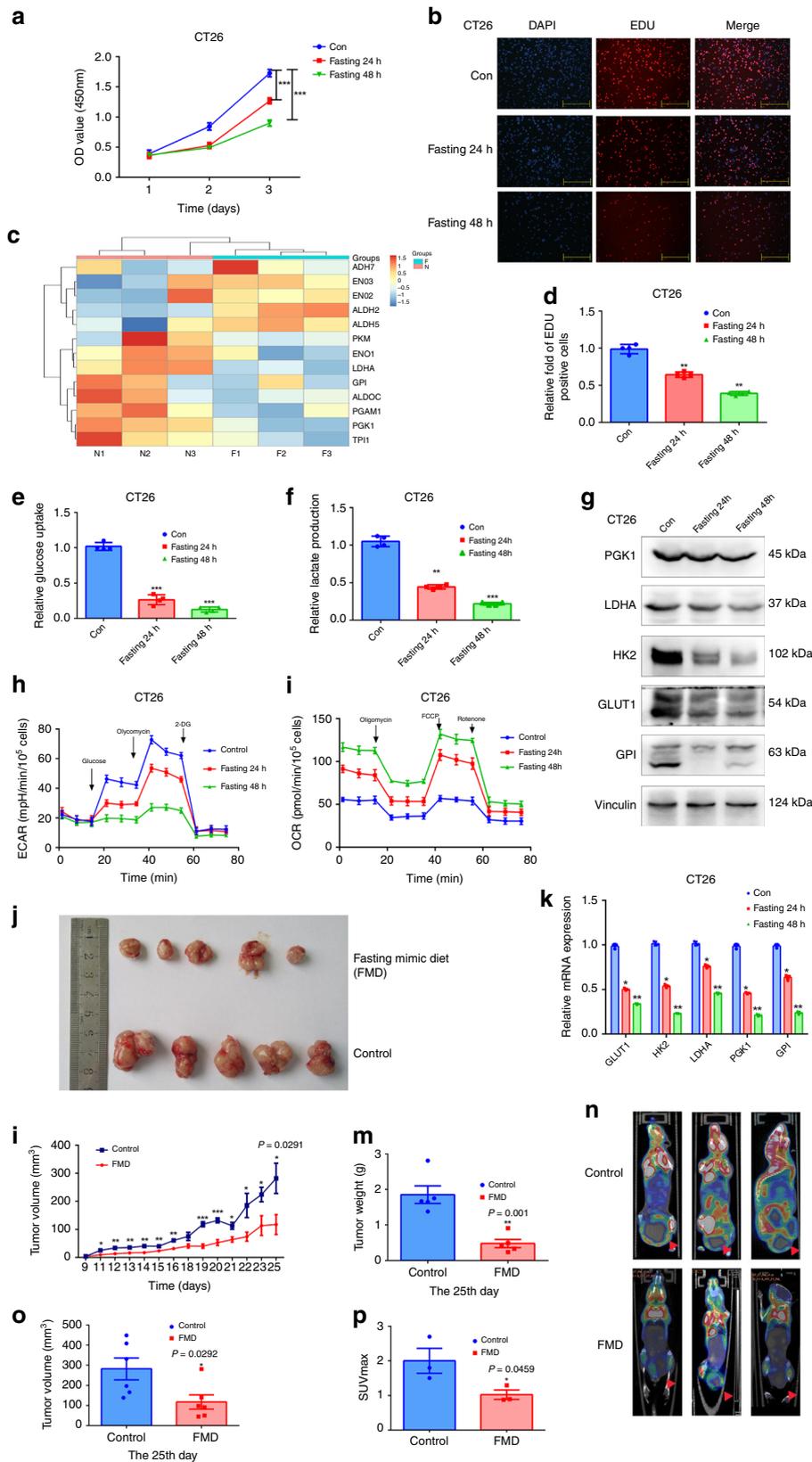
Fasting impairs glycolysis and inhibits proliferation in CRC. To explore the effect of fasting on the proliferation of CRC cells,

we examined cell proliferation by using a Cell Counting Kit-8 (CCK8) and EdU assays. Fasting significantly inhibited CRC cell proliferation in the CCK8 assay (Fig. 1a; Supplementary Fig. 2a). In the EdU immunofluorescence staining assay, the fasting group contained a lower relative fold fraction of EdU-positive cells than the control group (Fig. 1b, d; Supplementary Fig. 2b, d). To further investigate the effect of fasting on cell invasion, a Transwell assay was performed. Fasting markedly inhibited CT26 cell invasion (Supplementary Fig. 1a, b). Moreover, to explore the role of fasting in the cell cycle and apoptosis distribution, flow cytometry was performed. Our results demonstrated that fasting-induced cell cycle arrest in the G0/G1 and G2/M phases and induced apoptosis (Supplementary Figs. 1c, d, 2c, e; Supplementary Figs. 28, 29), which probably explains why fasting inhibits the proliferation of CRC cells.

To further assess the effect of fasting on the proliferation of CRC, an 8-plex iTRAQ proteomic technique and bioinformatics analysis were performed (Fig. 1c; Supplementary Figs. 3a, 4a, b). The heatmap showed 111 differentially upregulated genes and 168 differentially downregulated genes between the control and fasting groups. Gene Ontology analysis of the differentially expressed genes (DEGs) was carried out (Supplementary Fig. 5a–c). Pathways in the Kyoto Encyclopedia of Genes and Genomes (KEGG) that were enriched in DEGs indicated that the “Glycolysis/gluconeogenesis” pathway was highly downregulated (Supplementary Fig. 6a, b; Fig. 1c). To validate the impact of fasting on glucose metabolism, we examined glucose uptake and lactate production, two primary indicators of the Warburg effect. As expected, fasting reduced glucose uptake and lactate production in cells (Fig. 1e, f; Supplementary Fig. 2g, h). The extracellular acidification rate (ECAR), which is another indicator of glycolysis, was reduced in cells cultured in the fasting mimic medium (Fig. 1h; Supplementary Fig. 2j). The oxygen consumption rate (OCR), which reflects mitochondrial respiration, was increased in the fasting mimic medium (Fig. 1i; Supplementary Fig. 2k). Aerobic glycolysis was accompanied by the activation of a series of glycolytic genes. Therefore, several key rate-limiting enzymes in glucose metabolism were examined. The transcription and expression of rate-limiting enzymes in glucose metabolism (*GLUT1*, *HK2*, *LDHA*, *PGK1*, and *GPI*) were downregulated in CT26 and SW620 cells cultured in the fasting mimic medium (Fig. 1g, k; Supplementary Fig. 2f, i). Our data indicated that fasting plays a vital role in inhibiting glycolysis in CRC cells.

To further verify the effect of fasting on glucose metabolism observed in vitro, we subcutaneously injected CT26 cells into BALB/c mice. When the tumors were palpable, the mice were randomly assigned to a control or the fasting mimic diet (FMD) group. The FMD appreciably attenuated tumor growth in the mice (Fig. 1j, l). The final tumor weights and volumes in the fasting group were markedly lower than those in the control group (Fig. 1m, o). Furthermore, we used an ¹⁸F-fluorodeoxyglucose (¹⁸F-FDG) microPET/CT imaging system to assess the role of fasting in glucose metabolism. Consistent with the results in vitro, fasting dramatically inhibited ¹⁸F-FDG uptake in the in vivo xenograft model (Fig. 1n, p). Weight profiles during the normal diet and FMD cycle are shown in Supplementary Fig. 7. Taken together, these results suggested that fasting impairs glycolysis and inhibits proliferation in CRC.

***FDFT1* is upregulated by fasting and correlates with prognosis in CRC.** To further explore the effect of fasting on the proliferation of CRC cells, the GSE60653 data set²⁸ (from a study on fasting-induced anti-Warburg effects in CRC) was analyzed to identify DEGs between the control and fasting groups (Supplementary Figs. 8a, b and 9a, b). Gene Ontology and KEGG



pathway analyses for the DEGs were performed using FunRich software (<http://www.funrich.org>). Surprisingly, the most enriched biological pathway and biological process were the “Cholesterol biosynthesis” pathway and the “Energy pathway” and “Metabolism” processes (Supplementary Fig. 9c–f). Via the Database for Annotation, Visualization and Integrated Discovery

(DAVID, <https://david.ncicrf.gov/>), the top significantly enriched biological process and KEGG pathway were the “Cholesterol biosynthetic process” and the “Steroid biosynthesis pathway”, respectively (Supplementary Fig. 10a, b). *FDFT1* acts at the beginning of the “Steroid biosynthesis” pathway. Therefore, we chose the *FDFT1* as our hub gene for further research. First, we

Fig. 1 Fasting impairs glycolysis and proliferation of CT26 cells in vitro and in vivo. Fasting inhibited CT26 cell proliferation as measured by a CCK8 assay (from left to right: $P = 0.0009$; $P = 0.0006$). **b** Cell proliferation was also evaluated using EdU immunofluorescence staining. Proliferating cells were labeled with EdU. $n = 3$; scale bar: 100 μm . **c** Bioinformatics analysis of differentially expressed genes identified via iTRAQ proteomics. We magnified the genes related to the glycolysis pathway particularly. **d** The graph shows the relative fold fraction of EdU-positive cells. **e** Fasting reduced glucose uptake in CT26 cells. **f** Fasting decreased lactate production via glycolysis in CT26 cells. **g** Fasting downregulated the expression of rate-limiting glycolytic enzymes in glucose metabolism (*GLUT1*, *HK2*, *LDHA*, *PGK1*, and *GPI*) by western blot. **h** ECAR, an indicator of glycolysis, was reduced in CT26 cell cultured in the fasting mimic medium. **i** OCR, which reflects mitochondrial respiration, was increased in CT26 cell cultured in the fasting mimic medium. **j** CT26 cells were injected into BALB/c mice. When the tumors were palpable, the mice were randomly assigned to the control group or the fasting mimic diet (FMD) group. Photograph of dissected tumors (upper: FMD group; lower: control group; $n = 5$). **k** Fasting downregulated the transcription of rate-limiting glycolytic enzymes in glucose metabolism (*GLUT1*, *HK2*, *LDHA*, *PGK1*, and *GPI*) by qRT-PCR. **l** The tumor volumes were measured every day after the 9th day. The FMD attenuated tumor growth in mice ($n = 5$). **m, o** Tumor weights and tumor volumes on the 25th day ($n = 5$; $P = 0.001$; $P = 0.0292$). **n** Representative ^{18}F -FDG microPET/CT imaging of tumor-bearing mice ($n = 3$) (upper: control group; lower: FMD group). The tumors are indicated with arrows. **p** The ratio of the tumor SUVmax in the control group and the FMD group ($n = 3$; $P = 0.0459$). Error bars, mean \pm SD, the data are from three independent experiments. Two-sided *t* tests. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, compared with the control group.

validated that fasting can upregulate *FDFT1* expression. In the GSE60653 data set, the expression of *FDFT1* was increased significantly in the fasting group compared with that in the control group (Fig. 2a). Furthermore, in the iTRAQ proteomics analysis, the relative expression of *FDFT1* was greatly elevated in the fasting group compared with that in the control group (Fig. 2b). In addition, the mRNA expression of *FDFT1* in dissected tumor samples from the fasting mimic group and the control group was measured by qRT-PCR. The mRNA expression of *FDFT1* was markedly increased in the fasting group (Fig. 2c), and western blotting indicated that fasting mimic medium increased the protein level of *FDFT1* in cells (Fig. 2d, e). Our results thus showed that fasting upregulates the expression of *FDFT1* in CRC.

The expression of *FDFT1* was compared in 23 human CRC tissues and matched adjacent noncancerous tissues, by immunohistochemical (IHC) staining and qRT-PCR. The expression of *FDFT1* was downregulated and lower in most of the tumor tissues (19/23), but upregulated in most of the adjacent noncancerous tissues (18/23) (Fig. 2f, g). The relative expression levels of *FDFT1* mRNA was also assessed in 81 CRC tissues and matched adjacent noncancerous tissues. The levels of *FDFT1* in CRC tissues were dramatically lower than those in noncancerous tissues (Fig. 2h). We further examined *FDFT1* expression in CRC cell lines (DLD1, HCT116, SW620, SW480, and CT26) and the colorectal mucosal epithelial cell line NCM460 by qRT-PCR. As expected, the expression of *FDFT1* was also appreciably decreased in the CRC cell lines compared with NCM460 cells (Supplementary Fig. 11a), consistent with the results in Cancer Cell Line Encyclopedia (CCLE) database (Supplementary Fig. 11b, c). Therefore, *FDFT1* is downregulated in CRC tissues and cell lines.

To further determine the role of *FDFT1* in CRC, we assessed the association between *FDFT1* expression and clinicopathological features in patients with CRC. The median expression level was used as the cutoff. The low expression of *FDFT1* was significantly associated with tumor size, histological type, lymph node metastasis, tumor differentiation, invasion, distant metastasis, and clinical stage (Table 1). However, no significant association was found between *FDFT1* expression and age, gender, tumor location, or carcinoembryonic antigen (CEA) level. These findings indicated that *FDFT1* downregulation is involved in the malignant progression of CRC. To further evaluate the relationship between *FDFT1* expression and the survival time of CRC patients, a Kaplan–Meier analysis was performed. Our data showed that high *FDFT1* expression predicts better prognoses for patients with CRC in the Fudan University Shanghai Cancer Center (FUSCC) cohort ($P = 0.0238$, log-rank test) (Fig. 2i).

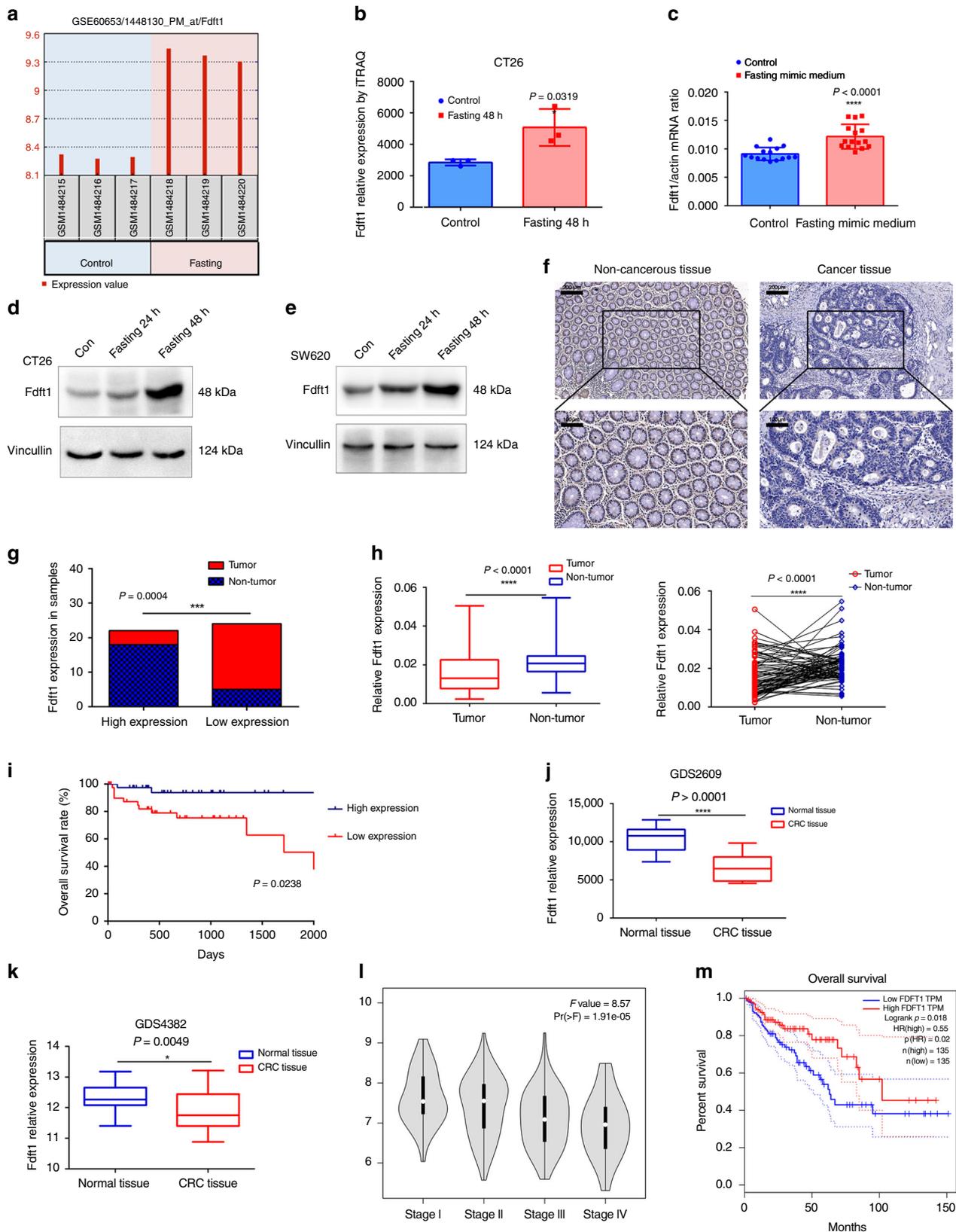
Moreover, to further validate the role of *FDFT1* in CRC, we used GEO and Gene Expression Profiling Interactive Analysis (GEPIA) databases to analyze TCGA data sets. The expression of

the *FDFT1* gene was significantly lower in CRC tissues than in normal tissues in the GDS2609 and GDS4382 data sets (Fig. 2j, k). Furthermore, the GEPIA database (<http://gepia.cancer-pku.cn/>) indicated lower *FDFT1* correlated with higher TNM stage ($P = 1.91 \times 10^{-5}$) in CRC patients (Fig. 2l). The survival analysis of the data from the TCGA data set indicated that high *FDFT1* expression was associated with better prognosis ($P = 0.018$, log-rank test) (Fig. 2m). These results were consistent with our results in the FUSCC cohort. Altogether, these results indicated that *FDFT1* was downregulated in CRC tissues, and was correlated with malignant progression and poor prognosis in patients with CRC.

Subsequently, to gain a deeper understanding of its mechanism, we studied the role of sterol regulatory element-binding protein-2 (*SREBP2*), a key transcriptional regulator of metabolic genes. The results showed that fasting simulation increased the protein and mRNA levels of *SREBP2* in CRC cells (Supplementary Fig. 12a–c). To assess the biological function of *SREBP2* in CRC, we used lentiviral-mediated *SREBP2* overexpression and knockdown in CT26 cells (Supplementary Fig. 12d, e). We also performed a colony-formation assay when overexpressing or knocking down *SREBP2*, and the results showed that *SREBP2* overexpression decreased, whereas *SREBP2* knockdown increased colony-formation capacity (Supplementary Fig. 12f, g). Then, we examined the protein and mRNA levels of *FDFT1* when overexpressing or knocking down *SREBP2*, and found that overexpression of *SREBP2* upregulated *FDFT1* and vice versa, moreover, the overexpression of *SREBP2* was more pronounced during fasting simulation (Supplementary Fig. 12h, i). Subsequently, we used a cloning assay to detect whether *SREBP2* reverses cell proliferation caused by knockdown of *FDFT1* in CT26 (Supplementary Fig. 12j, k). In conclusion, these results indicated that *FDFT1* played a role in reducing the proliferation of CRC cells under the action of *SREBP2*.

***FDFT1* negatively regulates the proliferation of CRC cells.** To assess the biological function of *FDFT1* in CRC, lentivirus-mediated overexpression and knockdown of *FDFT1* were performed in CT26 and SW620 cells. Images of GFP expression in CRC cells after lentiviral infection were acquired with a fluorescence microscope (Supplementary Figs. 13a–16a). The efficiency of *FDFT1* overexpression (Fig. 3a, b; Supplementary Fig. 15b, c) and knockdown (Fig. 3c, d; Supplementary Fig. 16c, d) were effectively achieved in CT26 and SW620 cells, as indicated by the q-PCR and western blotting results.

To further investigate the effect of *FDFT1* on cell proliferation, CCK8, EdU, and colony-formation assays were conducted. *FDFT1* overexpression inhibited CRC cell proliferation (Fig. 3e; Supplementary Fig. 15d), whereas *FDFT1* knockdown promoted



it (Fig. 3f; Supplementary Fig. 16b). In EdU immunofluorescence staining assay, *FDFT1* overexpression resulted in a lower relative fold fraction of EdU-positive cells (Fig. 3g, h; Supplementary Fig. 15g, h), yet *FDFT1* knockdown resulted in a greater relative fold fraction of EdU-positive cells (Fig. 3i, j; Supplementary Fig. 16f, g). In addition, *FDFT1* overexpression decreased the

colony-forming capacity of CRC cells (Fig. 3k, l; Supplementary Fig. 15e, f), whereas *FDFT1* knockdown enhanced it (Fig. 3m, n; Supplementary Fig. 16e, h). To further investigate the effect of *FDFT1* on cell invasion, a Transwell assay was performed. *FDFT1* overexpression inhibited cell invasion (Fig. 3o, p), whereas *FDFT1* knockdown increased it (Fig. 3q, r). In addition, *FDFT1*

Fig. 2 Fasting upregulates the level of *FDFT1*, which is correlated with prognosis in CRC. **a** The expression of *FDFT1* was increased significantly in the fasting group compared with that in the control group in the GSE60653 data set ($n = 3$). **b** The relative expression of *FDFT1* was also increased greatly in the fasting group compared with that in the control group by iTRAQ ($n = 3$; $P = 0.0319$). **c** The mRNA expression of *FDFT1* in dissected tumor tissue from the fasting mimic group and the control group was measured by qRT-PCR ($n = 15$; $P < 0.0001$). **d, e** Fasting mimic medium also increased the protein level of *FDFT1* in CT26 and SW620 cells. **f** Representative graph of the IHC analysis carried out in human CRC and noncancerous tissues ($n = 23$; upper: scale bar is 200 μm ; lower: scale bar is 100 μm). **g** The expression of *FDFT1* was downregulated in most of the tumor tissues (19/23), but was upregulated in most of the adjacent noncancerous tissues (18/23) ($n = 23$; $P = 0.0004$). **h** The relative expression levels of *FDFT1* mRNA in CRC tissues and matched adjacent noncancerous tissues were determined by qRT-PCR ($n = 81$; both $P < 0.0001$). **i** Kaplan–Meier analysis of the overall survival of patients with CRC in the FUSCC cohort according to *FDFT1* expression. The median expression level was used as the cutoff. High *FDFT1* expression predicted better prognoses for CRC patients in the FUSCC cohort. (high *FDFT1* patients = 39, low *FDFT1* patients = 42; $P = 0.0238$, log-rank test) **j, k** The expression of the *FDFT1* gene was significantly lower in CRC tissues than in normal tissues in the GDS2609 and GDS4382 data sets ($P < 0.0001$; $P = 0.0049$). **l** Analysis of the correlation of *FDFT1* expression with TNM stage in CRC patients. Lower *FDFT1* expression was correlated with higher TNM stage ($P = 1.91 \times 10^{-5}$). **m** Survival analysis of *FDFT1* data from the TCGA database stratified by *FDFT1* expression. High *FDFT1* expression indicated a better prognosis. ($P = 0.018$, log-rank test). Error bars, mean \pm SD, the data are from three independent experiments. Two-sided t tests. Box denotes 25th to 75th percentile, horizontal bar is median in **h, j, and k**. Kaplan–Meier analysis and log-rank tests were used in panels **i, m**. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$, compared with the control group (or non-tumor/normal tissue).

Table 1 The relationship between *Fdft1* expression and clinicopathological features in 81 CRC patients from FUSCC.

Variable	Number	<i>Fdft1</i>		χ^2 test P-value
		Low expression	High expression	
Age (years)	<60	51	27	0.798
	≥ 60	30	15	
Gender	Female	60	33	0.338
	Male	21	9	
Tumor location	Colon	30	12	0.102
	Rectum	51	30	
Size	<5 cm	42	15	0.003*
	≥ 5	39	27	
Histological type	Adenocarcinoma	66	30	0.016*
	Mucinous adenocarcinoma	15	12	
Lymph node metastasis	No	42	12	0.000***
	Yes	39	30	
Tumor differentiation	Well, moderate	60	27	0.037*
	Poor and others	21	15	
Invasion	T ₁₋₂	21	6	0.013*
	T ₃₋₄	60	36	
Distant metastasis	No	75	36	0.043*
	Yes	6	6	
Clinical stage	I–II	30	9	0.003**
	III–IV	51	33	
CEA	< 5 ng/ml	54	24	0.059
	≥ 5 ng/ml	27	18	

Pearson's χ^2 tests were used. The results were considered statistically significant at $P < 0.05$. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

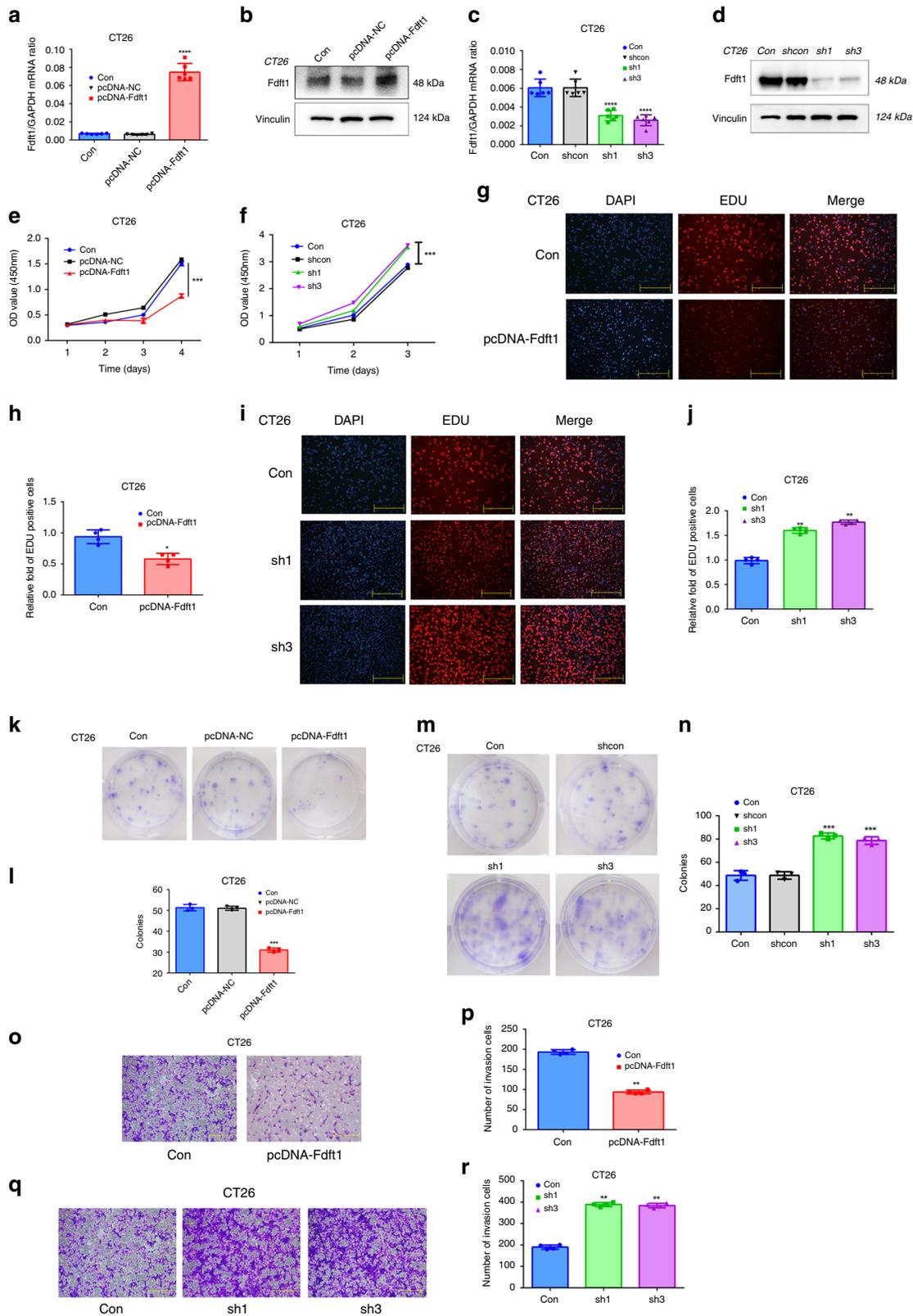
overexpression induced G0/G1 phase cell cycle arrest and apoptosis (Supplementary Figs. 13b, c and 15i, j), whereas *FDFT1* knockdown induced S phase cell cycle arrest and attenuated apoptosis (Supplementary Figs. 14b, c and 16i, j). In summary, *FDFT1* overexpression inhibited cell proliferation and induced G0/G1 phase cell cycle arrest and apoptosis, while *FDFT1* knockdown promoted cell proliferation, induced S phase cell cycle arrest, and attenuated apoptosis in CRC cells.

We also extend our experiments to PIK3CA-Mut cell line (HCT116 and HT29) and the human colorectal mucosal epithelial cell line NCM460 to see whether fasting or *FDFT1* have effects on cell proliferation. The results showed that the effect of fasting and *FDFT1* on PIK3CA-Mut cell lines (HCT116 and HT29) proliferation were similar to that in the previous PIK3CA-WT cell lines (CT26 and SW620) (Supplementary Fig. 17a–p), but *FDFT1* had no effect on NCM460 proliferation (Supplementary Fig. 18a–d).

***FDFT1* is an important downstream target of fasting in CRC.**

We further evaluated whether the inhibitory effect of fasting on CRC increases when combined with *FDFT1* overexpression. Our data demonstrated that compared with either treatment alone, *FDFT1* overexpression combined with fasting had the greatest inhibitory effect on CRC cell proliferation (Fig. 4a; Supplementary Fig. 19c). Moreover, an EdU assay showed that *FDFT1* overexpression combined with fasting yielded the most marked reduction in the proliferative capacity of CRC cells (Supplementary Fig. 19a, b, d, e). Furthermore, we studied *FDFT1* protein levels in four groups in vitro. Western blotting indicated that fasting and *FDFT1* overexpression increased the protein level of *FDFT1* in CRC cells. Fasting exerted an additive effect on *FDFT1* expression level in cells overexpressing *FDFT1* in the suppression of CRC cell proliferation (Fig. 4b).

To further confirm the effect of combining *FDFT1* overexpression with fasting on cell proliferation observed in vitro, we



subcutaneously injected CT26 cells and *FDFT1*-overexpressing CT26 cells into BALB/c mice. Our results indicated that both the FMD and *FDFT1* overexpression inhibited tumor growth in the mice. Compared with FMD alone or *FDFT1*-overexpressing alone, FMD combined with *FDFT1* overexpressing had the most dramatic inhibitory effect on tumor growth in the mice (Fig. 4c, d). Consistent with these results,

FMD combined with *FDFT1* overexpressing had the most significant inhibitory effect on ¹⁸F-FDG uptake in the in the xenograft model (Fig. 4e, f). In addition, the protein expression of *FDFT1* in dissected tumor samples evaluated by IHC indicated that either FMD or *FDFT1* overexpression with a normal diet increased the protein level of *FDFT1* in vivo. (Fig. 4g, h).

Fig. 3 **FDFT1 negatively regulates the proliferation of CRC cells.** **a, b** The efficiency of *FDFT1* overexpression in CT26 cells was measured by qRT-PCR and western blotting ($P < 0.0001$). **c, d** The efficiency of *FDFT1* knockdown in CT26 cells was measured by qRT-PCR and western blotting (both $P < 0.0001$). **e** *FDFT1* overexpression inhibited CT26 cell proliferation as measured by a CCK8 assay ($P = 0.0006$). **f** *FDFT1* knockdown increased CT26 cell proliferation as measured by a CCK8 assay (sh1 vs con: $P = 0.0008$; sh3 vs con: $P = 0.0009$). **g** Cell proliferation in control and *FDFT1*-overexpressing CT26 cells was also evaluated using EdU immunofluorescence staining. Scale bar: 100 μm . **h** The graph shows the relative fold fraction of EdU-positive cells. **i** Cell proliferation was also evaluated in control and *FDFT1* knockdown CT26 cells using EdU immunofluorescence staining. Scale bar: 100 μm . **j** The graph shows the relative fold fraction of EdU-positive cells. **k** *FDFT1* overexpression decreased the colony-forming capacity of CT26 cells as measured by a colony-formation assay. **l** The graph shows the statistical results of the colonies. **m** *FDFT1* knockdown increased the colony-forming capacity of CT26 cells as measured by a colony-formation assay. **n** The graph shows the statistical results of the colonies (from left to right: $P = 0.0003$; $P = 0.0006$). **o** *FDFT1* overexpression inhibited CT26 cell invasion as measured by a Transwell assay. Scale bar: 100 μm . **p** The graph shows the number of invaded cells. **q** *FDFT1* knockdown increased CT26 cell invasion as measured by a Transwell assay. Scale bar: 100 μm . **r** The graph shows the number of invaded cells. Error bars, mean \pm SD, the data are from three independent experiments. Two-sided *t* tests. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$, compared with the control group.

Our previous data showed that fasting upregulated the expression of *FDFT1* and *FDFT1* acted as a tumor suppressor in CRC. Our data also suggested that fasting synergizes with *FDFT1* overexpression in the inhibition of CRC proliferation in vitro and in vivo. To evaluate whether the inhibitory effect of fasting on CRC is mediated by *FDFT1*, we assessed whether *FDFT1* knockdown would reverse the inhibitory effect of fasting on CRC. Our data demonstrated that *FDFT1* knockdown combined with fasting reversed the inhibitory effect of fasting on CRC cell proliferation (Fig. 4j; Supplementary Fig. 20c). Moreover, an EdU assay showed that *FDFT1* knockdown combined with fasting abrogated the fasting inhibition of CRC cell proliferation (Supplementary Fig. 20a, b, d, e).

To further confirm our in vitro observation, we subcutaneously injected CT26 cells and *FDFT1*-knockdown CT26 cells into BALB/c mice. When the FMD was combined with the implantation of *FDFT1* knockdown CT26 cells in vivo, the inhibitory effect of fasting on CRC tumor growth was reversed (Fig. 4j, k). Overall, these results demonstrated that *FDFT1* was an important downstream target of fasting that mediates the inhibition of CRC cell proliferation.

The mTOR level is inversely correlated with *FDFT1* level in CRC. To identify the core signaling pathway underlying the inhibitory effect of *FDFT1* on the proliferation of CRC cells, the 8-plex iTRAQ proteomic technique and bioinformatics analysis were performed again. The most enriched pathways involving DEGs between *FDFT1* knockdown and control CT26 cells included the “mTOR signaling” and “Glycolysis” pathways in Ingenuity Pathway Analysis (IPA) (Supplementary Fig. 21a). The most enriched pathways involving DEGs between *FDFT1*-overexpressing and control CT26 cells included the “mTOR signaling” and “Oxidative phosphorylation” pathways in IPA (Supplementary Fig. 21b). We speculated that *FDFT1* inhibited the mTOR-related pathway, thereby suppressing glycolysis in CRC cells. First, we investigated the correlation between *FDFT1* and mTOR. mTOR protein levels decreased following *FDFT1* overexpression, but increased following *FDFT1* knockdown (Fig. 5a). Our results suggested that *FDFT1* expression is inversely correlated with mTOR expression. To further confirm our observation, the expression of *FDFT1* and mTOR was examined by IHC staining in parallel human CRC specimens from FUSCC (Fig. 5b). Patients with high *FDFT1* expression had low mTOR expression, which increased the validity of our previous results. Therefore, our data implied that *FDFT1* expression was negatively correlated with mTOR expression, and that mTOR was a potential downstream target of *FDFT1* in CRC.

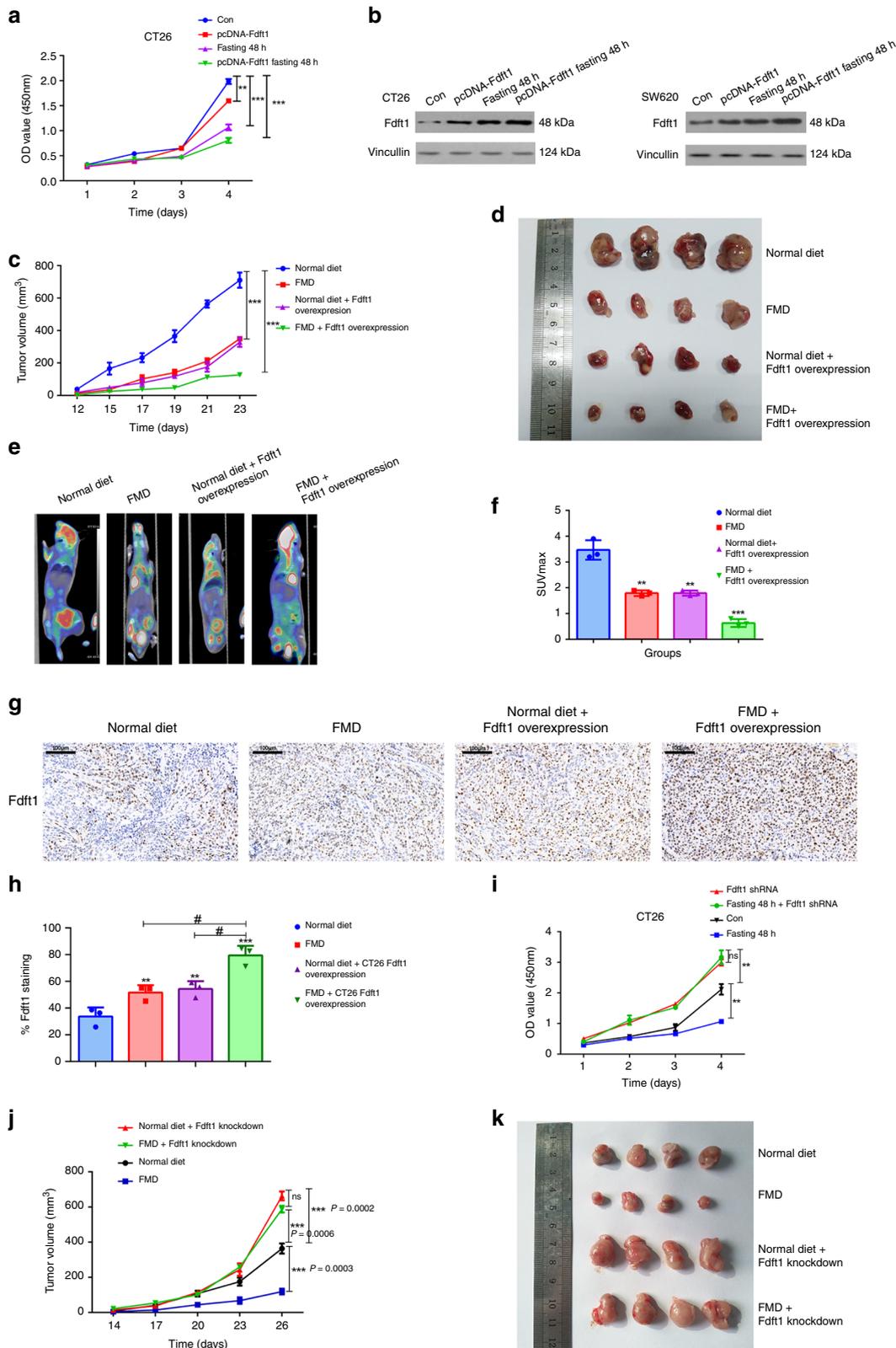
To make the link between *FDFT1* and mTOR stronger, we evaluated the effect of mTOR silencing on *FDFT1* expression level and whether treatment with an mTOR inhibitor would reverse the

effects of *FDFT1* knockdown. First, we transfected CT26 and SW620 cells with siRNA targeting mTOR (Fig. 5c). Our results indicated that mTOR silencing increased the *FDFT1* expression level in CT26 cell (Fig. 5d). An mTOR inhibitor prevents an increase in mTOR protein levels in *FDFT1* knockdown cells (Fig. 5e). Moreover, an mTOR activator prevents an increase in *FDFT1* protein levels in *FDFT1* overexpression cells, identifying an inverse relationship between *FDFT1* and mTOR (Supplementary Fig. 22a). Meanwhile, phosphorylation of two mTOR downstream target proteins, S6k and S6, were decreased under fasting or *FDFT1* overexpression in colorectal cells (Fig. 5f; Supplementary Fig. 22b).

To explore the function of mTOR in CRC, we examined the influence of mTOR on CRC cell proliferation by CCK8 and EdU assays and found that the silencing of mTOR decreased cell proliferation (Fig. 5g, h). In the EdU immunofluorescence staining assay, the silencing of mTOR resulted in a lower relative fold fraction of EdU-positive cells (Supplementary Fig. 22c–f). These data showed that mTOR was a positive regulator of CRC cell proliferation.

Next, the impact of mTOR on glycolysis in CRC cells was assessed. Silencing mTOR reduced glucose uptake and lactate production in CRC cells (Fig. 5k, n). Furthermore, the silencing of mTOR decreased the ECAR, but increased the OCR of CT26 and SW620 cells (Fig. 5i, j, l, o). In addition, we examined the protein expression of AKT, HIF1 α , and relevant glycolytic genes by western blotting. As expected, the silencing of mTOR decreased the expression of AKT, HIF1 α , and proteins encoded by relevant glycolytic genes, such as GLUT1, HK2, LDHA, GPI, and PGK1 (Fig. 5m). Finally, we analyzed the correlation between mTOR expression and AKT, HIF1 α , GLUT1, HK2, and GPI expression in TCGA data sets. Consistent with the results of previous studies, a strong correlation was observed between mTOR expression and AKT1, HIF1 α , GLUT1, HK2, and GPI expression (Fig. 5p–t). Therefore, these observations supported the hypothesis that mTOR positively regulates the aerobic glycolysis involved in CRC cell proliferation.

***FDFT1* inhibits the AKT-mTOR-HIF1 α pathway in CRC glycolysis.** Our iTRAQ proteomics analysis indicated that *FDFT1* is probably a negative regulator of glucose metabolism in CRC. Our results showed that *FDFT1* overexpression reduced glucose uptake and lactate production in CT26 and SW620 cells (Fig. 6a, b; Supplementary Fig. 23a, b). Subsequent analysis indicated that in cells overexpressing *FDFT1*, ECAR was reduced, but OCR was increased (Fig. 6c, d; Supplementary Fig. 23c, d). In contrast, *FDFT1* knockdown increased glucose uptake and lactate production (Fig. 6e, f; Supplementary Fig. 23e, f). Moreover, in *FDFT1* knockdown, ECAR was increased, but OCR was decreased (Fig. 6g, h; Supplementary Fig. 23g, h). Furthermore, *FDFT1* overexpression inhibited the protein and mRNA expression of mTOR-targeted glycolytic enzymes, including GLUT1, HK2,



PGK1, *GPI*, and *LDHA* (Fig. 6i, m; Supplementary Fig. 23i, m). In contrast, *FDFT1* knockdown increased the protein and mRNA expression of *mTOR*-targeted glycolytic enzymes, including *GLUT1*, *HK2*, *PGK1*, *GPI*, and *LDHA* (Fig. 6j, m; Supplementary Fig. 23j, m). These results confirmed that *FDFT1* was a negative regulator of glucose metabolism in CT26 and SW620 cells.

Because the *AKT-mTOR-HIF1 α* pathway is an essential pathway that governs glycolysis and proliferation in CRC and *FDFT1* expression is inversely correlated with *mTOR* expression, we decided to determine whether *FDFT1* is negatively correlated with the *AKT-mTOR-HIF1 α* pathway. Notably, *FDFT1* overexpression decreased the protein and mRNA expression of *AKT*, *mTOR*, and *HIF1 α* in CRC cells (Fig. 6k, n; Supplementary

Fig. 4 FDFT1 is a downstream target of fasting in suppressing CRC proliferation. **a** *FDFT1* overexpression and fasting for 48 h inhibited CT26 cell proliferation as measured by a CCK8 assay. Compared with either treatment alone, *FDFT1* overexpression combined with fasting for 48 h had the most obvious inhibitory effect on CT26 cell proliferation (from left to right: $P = 0.0021$; $P = 0.0005$; $P = 0.0003$). **b** Western blotting indicated that fasting 48 h and *FDFT1* overexpression increased the protein level of *FDFT1* in CRC cells. Fasting exerted an additive effect on *FDFT1* expression level in cells overexpressing *FDFT1* in the suppression of CRC cell proliferation. **c, d** Photograph of dissected tumors (first line: CT26 cells + normal diet; second line: CT26 cells + FMD; third line: *FDFT1*-overexpressing CT26 cells + normal diet; fourth line: *FDFT1*-overexpressing CT26 cells + FMD; $n = 4$; both $P < 0.0001$). Both the FMD and *FDFT1* overexpression inhibited tumor growth in the mice. The FMD combined with the implantation of *FDFT1*-overexpressing CT26 cells had the most obvious inhibitory effect on tumor growth in the mice. **e** Representative ^{18}F -FDG microPET/CT imaging of tumor-bearing mice. **f** The ratio of the tumor SUVmax in the four groups. The SUVmax was decreased most significantly in the *FDFT1*-overexpressing CT26 cells + FMD group ($n = 3$; from left to right: $P = 0.0018$; $P = 0.0018$; $P = 0.0003$). **g** The protein expression of *FDFT1* in dissected tumor samples was evaluated by IHC. Scale bar: 100 μm . **h** Graph shows the quantitative analysis of *FDFT1* staining ($n = 3$). **i** The effect of *FDFT1* knockdown, fasting 48 h and *FDFT1* knockdown combined with fasting 48 h on CT26 cell proliferation was evaluated by CCK8 (upper: $P = 0.005$; lower: $P = 0.0045$). **j, k** Photograph of dissected tumors (first line: CT26 cells + normal diet; second line: CT26 cells + FMD; third line: sh*FDFT1* CT26 cells + normal diet; fourth line: sh*FDFT1* CT26 cells + FMD; $n = 4$; $P = 0.0006$; $P = 0.0002$; $P = 0.0003$). The FMD inhibited tumor growth in mice. *FDFT1* knockdown promoted tumor growth in mice. The FMD combined with sh*FDFT1* CT26 cells did not inhibit tumor growth in the mice. Error bars, mean \pm SD, the data are from three independent experiments. Two-sided *t* tests. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, compared with the control group (or normal diet group). # $P < 0.05$, ## $P < 0.01$.

Fig. 16k, n). In contrast, *FDFT1* knockdown increased the protein and mRNA expression of *AKT*, *mTOR*, and *HIF1 α* (Fig. 6l, n; Supplementary Fig. 23l, n). These results suggested that *FDFT1* inhibited glucose metabolism through suppressing the *AKT-mTOR-HIF1 α* pathway in CRC.

Because fasting and *FDFT1* upregulation reduced *mTOR*, *AKT*, and *HIF1 α* expression in vitro, we hypothesized that the effect of fasting may be due to a strong glucose reduction during FMD, so we added a group of FMD + glucose in vivo tumor formation experiment. In this group, glucose was added to drinking water in correspondence with the FMD. This group can reverse the tumor growth inhibition induced by the FMD (Fig. 6o, p). Compared with FMD group, the protein level of *FDFT1* and *mTOR* was reversed in FMD + glucose group (Fig. 6q). The glucose level in FMD + glucose mice was significantly higher than that of the FMD group (Fig. 6r).

We also examined the effect of fasting, *FDFT1* overexpression and fasting combined with *FDFT1* overexpression on the glycolysis and total cholesterol production in CRC cell lines and found that overexpression of *FDFT1* and fasting reduced glycolysis and total cholesterol levels. Meanwhile, overexpression of *FDFT1* combined with fasting had additive effects in reducing glycolysis and total cholesterol levels in CRC cell lines (Supplementary Fig. 24a–n). The mRNA level of key genes in cholesterol biosynthesis and efflux pathway were activated after fasting or *FDFT1* upregulation (Supplementary Fig. 25a–c).

Fasting and *mTOR* inhibitor synergize in suppressing CRC proliferation. We explored whether rapamycin, a pharmacological inhibitor of *mTOR*, can synergize with FMD in inhibiting the proliferation of CRC. The results indicated that both FMD and 1 mg/kg dose of rapamycin can robustly inhibit the proliferation of CRC and drastically improve survival (Fig. 7a–c). In addition, we found that rapamycin therapy could increase the levels of *FDFT1* protein and mRNA like fasting (Fig. 7d, e). Moreover, we also found that fasting and rapamycin synergize in delaying CRC progression, improving survival, and upregulating *FDFT1* (Fig. 7a–e). Weight profile in four groups is shown in Supplementary Fig. 26. Overall, these results demonstrated that fasting and rapamycin can be potential therapeutic implications to inhibit the proliferation of CRC.

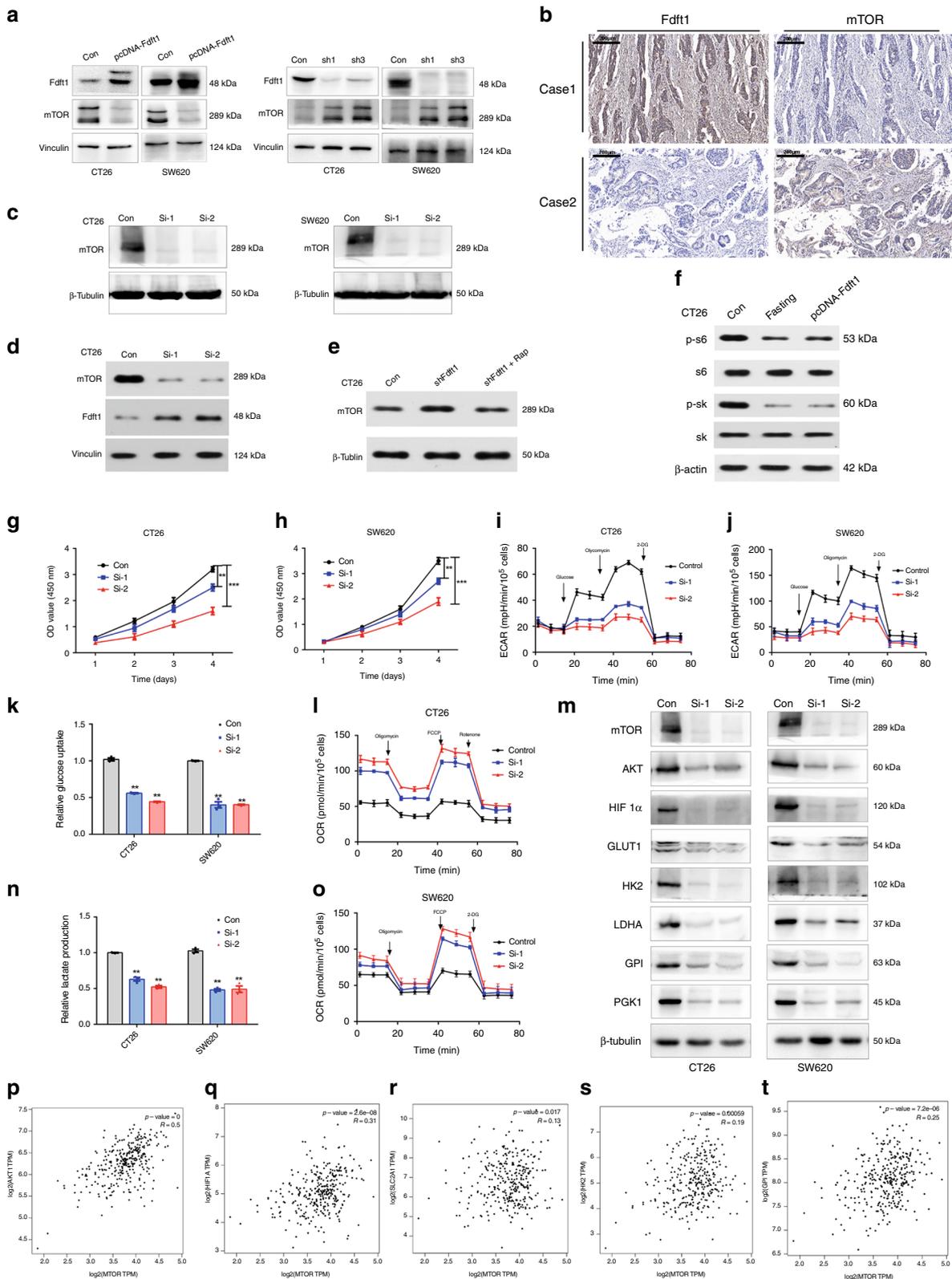
Clinical significance of the *FDFT1/AKT-mTOR-HIF1 α* pathway in CRC patients. To further validate our observation, we examined the clinical significance of *AKT1*, *mTOR*, *HIF1 α* , *GLUT1*, and *HK2* expression with *FDFT1* in CRC by analyzing the TCGA

data set. Because we speculated *FDFT1* as a tumor suppressor in CRC, we assessed the expression of *FDFT1* with that of *AKT1*, *mTOR*, *HIF1 α* , *GLUT1*, and *HK2*. The patients with a high expression of *FDFT1* and a low expression of *AKT1*, *mTOR*, *HIF1 α* , *GLUT1*, and *HK2* exhibited longer survival than those with a low expression of *FDFT1* and a high expression of the *AKT-mTOR-HIF1 α* pathway and glycolytic genes (Fig. 7f–j; Supplementary Fig. 27).

Discussion

Mounting evidence indicates that fasting exerts extensive anti-tumor effects in various cancers^{8,29,36,37}. However, the mechanism by which fasting inhibits CRC remains unclear. Our results showed that fasting inhibits the malignant progression of CRC by impairing aerobic glycolysis. In particular, our in vivo and in vitro experiments showed that fasting could dramatically elevate the expression of the cholesterologenic gene *FDFT1*. Moreover, we showed that *FDFT1* played an important tumor-suppressive role with clinical significance and function in CRC, and was also an important downstream target of fasting. Mechanistically, *FDFT1* performs its tumor-inhibitory function on glucose metabolism by negatively regulating *AKT/mTOR/HIF1 α* signaling. Furthermore, the pharmacological *mTOR* inhibitor rapamycin can synergize with FMD in inhibiting the proliferation of CRC. We conclude that fasting negatively regulates glucose metabolism and cell proliferation via the *FDFT1/AKT-mTOR-HIF1 α* axis in CRC (Fig. 7k).

Cancer cells usually exhibit aberrant metabolism resulting from metabolic reprogramming. The most prominent metabolic reprogramming occurring in cancer results in aerobic glycolysis in preference to mitochondrial oxidative phosphorylation, which provides continuous energy and nutrients to support uncontrolled proliferation; this reprogramming is termed the Warburg effect^{8,23,31,38}. Previous studies have demonstrated that caloric restriction or fasting can alter the overall metabolic state of cancer cells, including the dependence on aerobic glycolysis^{8,11,39,40}. In this study, we provided evidence that fasting inhibits the proliferation of CRC cells. Proteomics analysis showed that the glycolysis pathway was highly downregulated during fasting. A series of aerobic glycolysis-related assays indicated that fasting plays a vital role in inhibiting glycolysis in CRC cells. The proteasome pathway also was downregulated during fasting, which can be another promising direction to explore^{41–43}. We confirmed these results in an in vivo xenograft model. Fasting dramatically inhibited ^{18}F -FDG uptake and attenuated tumor growth in this xenograft model. These results suggested that, similar to traditional cancer therapy, fasting can be a potential therapeutic



approach in CRC. Given the critical role of fasting in CRC glucose metabolism, we further explored the potential underlying mechanism and downstream effectors.

Some studies have suggested that the antitumor effect of fasting is mediated through the modulation of insulin-like growth factor (IGF)-1 or insulin, or through the enhancement of antitumor immunity^{15,16,37,44}. To investigate the downstream target of

fasting that mediates the inhibition of CRC cell proliferation, we analyzed the GSE60653²⁹ data set (from a study on fasting-induced anti-Warburg effects in CRC) to identify DEGs between the control and fasting groups. Intriguingly, the results indicated that fasting upregulates the “Steroid biosynthesis” pathway, and that *FDFT1* was dramatically upregulated. *FDFT1* acts at a branch point in the mevalonate pathway, and is the first specific enzyme

Fig. 5 mTOR expression is inversely correlated with FDFT1 expression. **a** *FDFT1* overexpression inhibited the protein level of *mTOR*, whereas *FDFT1* knockdown increased the protein level of *mTOR* in CT26 and SW620 cells. **b** *FDFT1* expression and *mTOR* expression were negatively correlated in CRC patient samples. Scale bar: 200 μ m. **c** The *mTOR* silencing efficiency of the siRNA in CT26 and SW620 cells was validated by western blotting. **d** The effect of *mTOR* silencing on *FDFT1* expression level in CT26 was evaluated by western blotting. **e** The protein level of *mTOR* when *FDFT1* knockdown combined with or without *mTOR* inhibitor in CT26. **f** The protein level of pS6k, S6k, pS6, and S6 under the effect of fasting and *FDFT1* overexpression in CRC cells. **g, h** CCK8 proliferation assays showed that the silencing of *mTOR* decreased the proliferation of CT26 and SW620 cells. **k, n** The silencing of *mTOR* reduced glucose uptake and lactate production in CT26 and SW620 cells. **i, j, l, o** The silencing of *mTOR* decreased the ECAR and increased the OCR in CT26 and SW620 cells. **m** The silencing of *mTOR* decreased the expression of *AKT*, *HIF1 α* , and proteins encoded by relevant glycolytic genes, such as *GLUT1*, *HK2*, *LDHA*, *GPI*, *PGK1*, in CT26 and SW620 cells. **p–t** Based on TCGA data set analysis, *mTOR* expression was positively correlated with *AKT1*, *HIF1 α* , *GLUT1*, *HK2*, and *LDHA* expression. Error bars, mean \pm SD, the data are from three independent experiments. Two-sided *t* tests. **P* < 0.05, ***P* < 0.01, ****P* < 0.001, compared with the control group.

in cholesterol synthesis, catalyzing the reaction that produces squalene synthase^{34,45}. Clinically, high *FDFT1* expression in CRC is associated with better prognosis in The Cancer Genome Atlas (TCGA) data sets. However, *FDFT1* has seldom been studied in the field of cancer research. Limited studies addressed *FDFT1* in prostate cancer³⁵, ovarian cancer⁴⁶, and lung cancer⁴⁷, but there is no information on the function of *FDFT1* in CRC. Therefore, we selected *FDFT1* as the target gene. Our study validated that fasting upregulates the expression of *FDFT1* in CRC cells both in vitro and in vivo. Then, we observed that the downregulation of *FDFT1* was correlated with malignant progression and poor prognosis in CRC in both the FUSCC cohort and TCGA data sets.

To our knowledge, the biological function of *FDFT1* in CRC has not been studied. Our study showed that *FDFT1* negatively regulates the proliferation of CRC cells, and acts as a tumor suppressor in CRC. Furthermore our data suggested that fasting synergizes with *FDFT1* overexpression in the inhibition of CRC cell proliferation in vitro and in vivo. However, when fasting was combined with *FDFT1* knockdown in vivo, the inhibitory effect of fasting on CRC was reversed, indicating that *FDFT1* was an important downstream target of fasting that mediated the inhibition of CRC cell proliferation.

To further identify the core signaling pathway underlying the inhibitory effect of *FDFT1* on the proliferation of CRC cells, another proteomics analysis was performed. Based on the bioinformatics results, we speculated that *FDFT1* inhibited the *mTOR*-related pathway, thereby suppressing glycolysis in CRC cells. *mTOR* is a conserved serine/threonine kinase that plays a key role in integrating multiple physiological stimuli to regulate cell growth and metabolic pathways^{27,28,40,48}. *mTOR* deregulation occurs in many human pathologies, including cancer, metabolic diseases, nervous system diseases, and inflammation^{49,50}. There are already many *mTOR* inhibitors for the treatment of human cancer, and many more have been evaluated in clinical trials^{51–55}. *mTOR* activates glycolysis through modulating the expression of the transcription factor HIF-1 α , indirectly upregulating the transcription of almost all glycolytic genes in tumor cell^{5,28,56}. Our results indicated that *FDFT1* expression is negatively correlated with *mTOR* expression. Consistent with the data in previous reports^{27,57–60}, our data showed that *mTOR* is a positive regulator of aerobic glycolysis and proliferation in CRC cells. HIF1 α is a key regulator of the Warburg effect and regulates the expression of a variety of metabolism-related proteins⁶¹. The correlation between *mTOR* and HIF1 α prompted us to validate that *FDFT1* could regulate glucose metabolism through the *AKT-mTOR-HIF1 α* pathway. Through the effect of fasting on glucose metabolism as well as on the connection among *mTOR* signaling, fasting and glucose metabolism have been reported. To our knowledge, the impact of *FDFT1* on inhibiting the Warburg effect has not been reported during fasting; thus, our results innovatively validated that *FDFT1* is a negative regulator of glucose

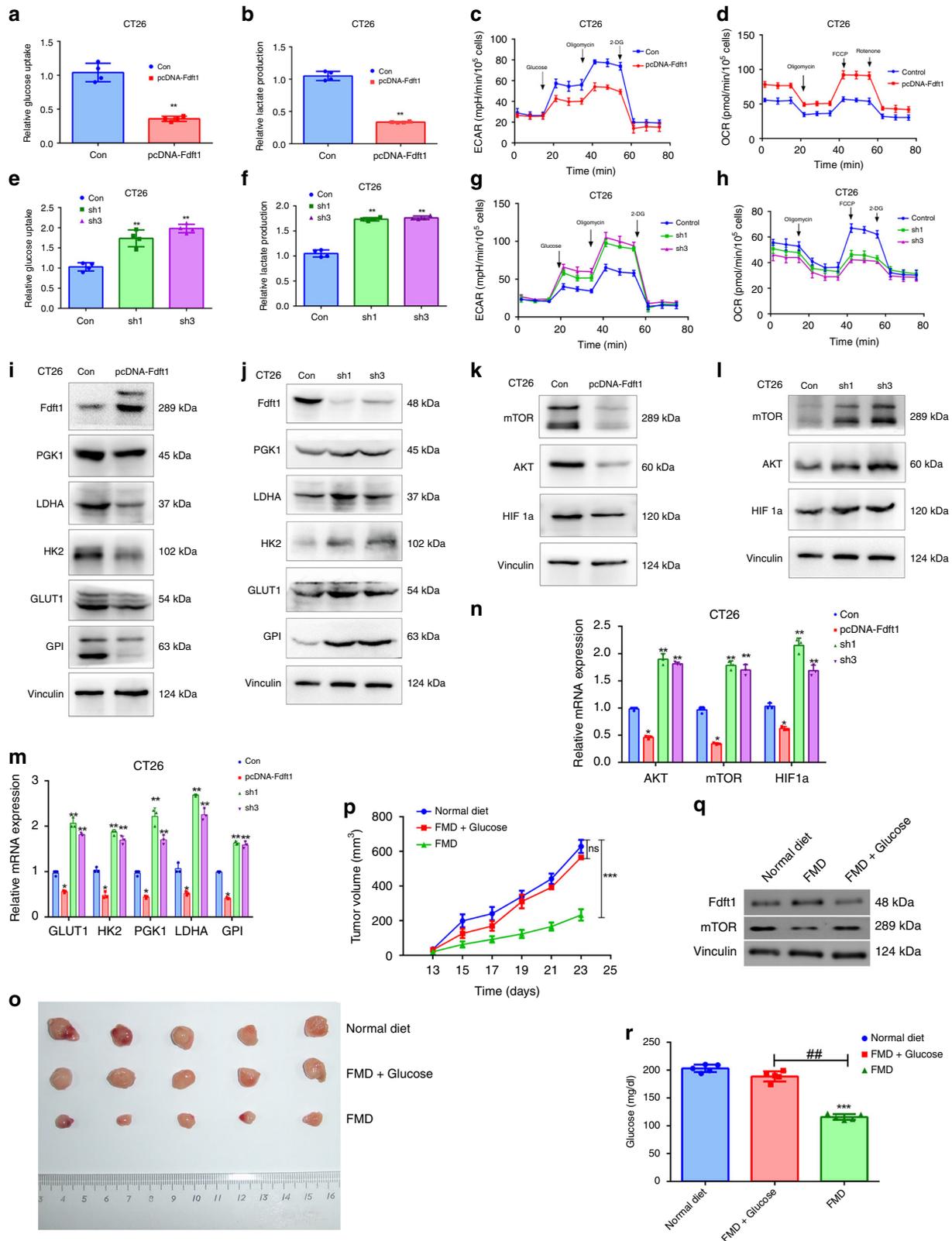
metabolism through suppressing the *AKT-mTOR-HIF1 α* pathway during fasting in CRC. As the clinical application of *FDFT1* will be challenging, we explored whether a pharmacological inhibitor of *mTOR* could be an effective therapy for colorectal cancer. Consistent with our in vitro observations, *mTOR* inhibitor can synergize with FMD in suppressing the proliferation of CRC. Moreover, patients with high *FDFT1* expression and low expression of the *AKT-mTOR-HIF1 α* pathway and glycolytic genes exhibited longer survival, adding validation to our hypothesis. The survival data also show a worse prognosis of *FDFT1*-low tumors regardless of the expression of other *mTOR* pathway genes, which suggest an alternative pathway for *FDFT1* to effect cancer proliferation potential. Several studies have found that cholesterol deprivation can inhibit tumor growth, decrease the phosphorylation of *AKT*, promote apoptosis⁶², decrease Bcl-xl, downregulate caspase 3 activation⁶³, or hinder entry of cells into the S phase⁶⁴. Our study showed that fasting and *FDFT1* overexpression reduced the total cholesterol production in CRC cell lines. So we agree there may be other pathways for *FDFT1* affect tumor growth. The mechanism by which *FDFT1* affects *mTOR* needs to be further explored. We will focus on studying these problems in the future.

In conclusion, we demonstrated that fasting was a negative regulator of glucose metabolism and proliferation via the *FDFT1/AKT-mTOR-HIF1 α* axis in CRC cells. A therapy based on *mTOR* inhibition could be a promising approach against CRC. These results indicated a good function of the cholesterologenic gene *FDFT1* in CRC glucose metabolism and suggest that *FDFT1* is a potential marker in CRC. Our results also elucidate potential therapeutic implications (involving fasting and *mTOR*) for CRC and indicate potential crosstalk between a cholesterologenic gene and glycolysis.

Methods

Cells and reagents. CRC cell lines CT26, SW620, HCT116, HT29, and human colorectal cancer mucosal epithelial cell line NCM460 were obtained from the American Type Culture Collection (ATCC; Shanghai, China) and cultured in DMEM (Biological Industries, USA) supplemented with 10% FBS (Gibco, USA). Isogenic PIK3CA mutant (HCT116 and HT29) were generated in advance^{65,66}. All culture media contained 100 U/ml penicillin and 100 mg/ml streptomycin and maintained at 37 °C in a humidified atmosphere containing 5% CO₂. The fasting mimic medium comprised of glucose-free DMEM (Gibco, USA) supplemented with 0.5 g/L glucose and 1% FBS; fasting was mimicked by incubating cells in this medium for 24 h or 48 h^{67,68}. To determine if *mTOR* can reverse *FDFT1* overexpression, pretreat CT26 and SW620 with *mTOR* activator MHY1485 (10 μ M) for 24 h.

Lentivirus production and stable cell line selection. The PGMLV-CMV-*FDFT1*-EF1-ZsGreen1-T2A-Puro (Genomeditech, Shanghai, China) plasmid was used to generate the *FDFT1* overexpression constructs. The PGMLV-hU6-*FDFT1*-CMV-ZsGreen1-PGK-Puro (Genomeditech) plasmid was used to generate the *FDFT1* shRNA constructs. The 21-bp sequences targeting *FDFT1* were GTGTTTAACTTCTGTGCTATT, GCAGGTATTCAAAGGAGTAGT, and GCCGTCAAAGCTATCATATAC. The PGMLV-CMV-SREBP2-EF1-ZsGreen1-T2A-Puro (Genomeditech) plasmid was used to generate the SREBP2 overexpression constructs. The



PGMLV-hU6-SREBP2-CMV-ZsGreen1-PGK-Puro (Genomeditech) plasmid was used to generate the SREBP2 shRNA constructs. The sequences targeting SREBP2 were ATGATGCGAGGCTGAGTTGTC and CCCTGGCTGTCTGTGTAATAC. Lentiviral particles were produced by transfecting the psPAX2 and pMD2.G plasmids into HEK293T cells using Lipofectamine 2000 (Invitrogen, USA) according to the manufacturer's protocol. Stable cell lines were obtained by infection with the lentiviral particles followed by puromycin selection. The efficiency of transfection was examined using real-time PCR and western blotting.

The siRNA transfection. We silenced *mTOR* expression in CRC cells by using siRNA-mediated silencing. The siRNAs targeting *mTOR* were 5'-CGAUCCAGUU GUCAUGGAAdTdT-3'/5'-UUCCAUGACAAUCUGGUAUCGdTdT-3', 5'-GAGAC UUGAUGGAAGAGAAAdTdT-3'/5'-UUCUCUCCAUCAAGUCUCdTdT-3', and 5'-GGUCGGAGUUUAAGGUCUAdTdT-3'/5'-UAGACCUAAAACUCCGACcd TdT-3' (Proteintech, Shanghai, China). siRNA duplexes targeting *mTOR* were transfected into colorectal cancer cells using Lipofectamine 2000 (Invitrogen, USA) in serum-free medium according to the manufacturer's instructions.

Fig. 6 FDFT1 inhibits glycolysis through suppressing the AKT-mTOR-HIF1 α pathway in CRC. **a** *FDFT1* overexpression reduced glucose uptake in CT26 cells. **b** *FDFT1* overexpression decreased lactate production via glycolysis in CT26 cells. **c** ECAR was reduced when *FDFT1* was overexpressed in CT26 cells. **d** OCR was increased when *FDFT1* was overexpressed in CT26 cells. **e** *FDFT1* knockdown increased glucose uptake in CT26 cells. **f** *FDFT1* knockdown increased lactate production via glycolysis in CT26 cells. **g** ECAR was increased when *FDFT1* was knocked down in CT26 cells. **h** OCR was decreased when *FDFT1* was knocked down in CT26 cells. **i, m** *FDFT1* overexpression inhibited the protein and mRNA expression of *mTOR*-targeted glycolytic enzymes, including *GLUT1*, *HK2*, *PGK1*, *GPI*, and *LDHA*, in CT26 cells. **j, n** *FDFT1* knockdown increased the protein and mRNA expression of *mTOR*-targeted glycolytic enzymes, including *GLUT1*, *HK2*, *PGK1*, *GPI*, and *LDHA*, in CT26 cells. **k, o** *FDFT1* overexpression decreased the protein and mRNA expression of *AKT*, *mTOR*, and *HIF1 α* . **l, p** *FDFT1* knockdown increased the protein and mRNA expression of *AKT*, *mTOR*, and *HIF1 α* . **o** Photograph of dissected tumors (the first line: normal diet, the second line: FMD + glucose, the third line: FMD, $n = 5$). **p** The tumor volumes were measured every 2 days after the 13th day. The FMD + glucose group can reverse the tumor growth inhibition induced by the FMD ($n = 5$; ns: $P = 0.1838$; $P = 0.0001$). **q** The protein level of *FDFT1* and *mTOR* in dissected tumor samples from normal diet group, FMD group and FMD + glucose group was measured by western blotting. **r** The glucose level in these three groups. Error bars, mean \pm SD, the data are from three independent experiments. Two-sided t tests. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, compared with the control group (or normal diet group). # $P < 0.05$, ## $P < 0.01$.

Cell proliferation assay. Cell proliferation was examined using a Cell Counting Kit-8 (CCK8; Dojindo Laboratories, Japan). Briefly, cell suspensions (3×10^3 /well) were seeded in 96-well culture plates and incubated for 5 days. CCK8 solution (10 μ L) was added to each well, and the cells were cultured for another 4 h. The optical density was measured at 450 nm using a microplate reader.

Colony-formation assay. Cells were seeded in triplicate in six-well plates at a density of 500 cells/well. After 14 days, most single colonies contained more than 50 cells. The cells were fixed with 4% paraformaldehyde for 20 min at room temperature, stained with 4 mg/mL crystal violet for 20 min, and counted under a light microscope (Leica DM IL, Germany).

EdU assay cells. In total, 1×10^5 cells from each group were seeded on coverslips and cultured for 24 h. Click-iT EdU Imaging Kits (#C10339, Invitrogen, USA) were used to label and detect the incorporated EdU according to the manufacturer's protocol. The staining results were observed under an inverted fluorescence microscope (IX51; Olympus, Tokyo, Japan).

Transwell migration assay. The Transwell migration assay was performed using 24-well cell culture inserts containing a transparent PET membrane (8.0- μ m pore size, #353097; BD Biosciences, USA). A total of 2×10^5 cells in 200 μ L serum-free DMEM were added to the upper chamber, and 800 μ L DMEM supplemented with 10% FBS was added to the lower chamber. Following 24 h of incubation, the migrated cells on the bottom of the membrane were fixed with 4% PFA for 20 min and stained with 0.1% Crystal violet for further analysis.

Cell cycle and apoptosis analysis. Cell cycle analysis was performed via propidium iodide (PI) staining following the manufacturer's protocols (Signalway Antibody, #CA002). To identify apoptotic cells, a PE Annexin V Apoptosis Detection Kit I (BD Biosciences, #559763) was used according to the manufacturer's protocol. The cells were analyzed by flow cytometry (Cell Lab Quanta, Beckman Coulter, USA).

Glycolysis analysis. Glucose Uptake Fluorometric Assay Kits (Biovision, #K666-100) and Lactate Colorimetric Assay Kits (Biovision, #K627-100) were purchased, and glycolysis was detected in CRC cells according to the manufacturer's protocols.

OCR and ECAR. Cellular mitochondrial function and cellular glycolytic capacity were measured by using a Seahorse Bioscience XF96 Extracellular Flux Analyzer according to the manufacturer's instructions for the Seahorse XF Glycolysis Stress Test Kit and Cell Mito Stress Test Kit (Seahorse Bioscience, USA). Briefly, 2×10^4 cells were seeded into 96-well cell culture XF microplates and incubated overnight for further testing. The ECAR and OCR values were calculated after normalization to the total cell number and are plotted as the mean \pm SD.

Protein extraction and western blot analysis. Briefly, total protein was extracted, qualified by BCA protein assay reagent, separated by SDS-PAGE, and detected by immunoblotting with specific antibodies. Antibodies against *FDFT1* (Abcam, ab195046), *mTOR* (Abcam, ab10268), *AKT* (Cell Signaling, #9272), vinculin (Cell Signaling, #4650), *HIF1 α* (Novus, NB100-105), *GLUT1* (HIF-Proteintech, 66290-1-Ig), *LDHA* (Proteintech, 19987-1-AP), *HK2* (Proteintech, 22029-1-AP), *PGK1* (Proteintech, 17811-1-AP), and *GPI* (Abcam, ab66340) were purchased from the designated manufacturers. Vinculin was used as the loading control.

RNA isolation and quantitative real-time PCR. The total RNA was extracted using TRIzol reagent (Invitrogen). A Takara PrimeScript RT reagent kit was used for reverse transcription to obtain cDNA. The expression of the candidate genes and GAPDH was assessed by quantitative real-time PCR using an ABI 7900HT

real-time PCR system (Applied Biosystems). The primer sequences are listed in Supplementary Table 1.

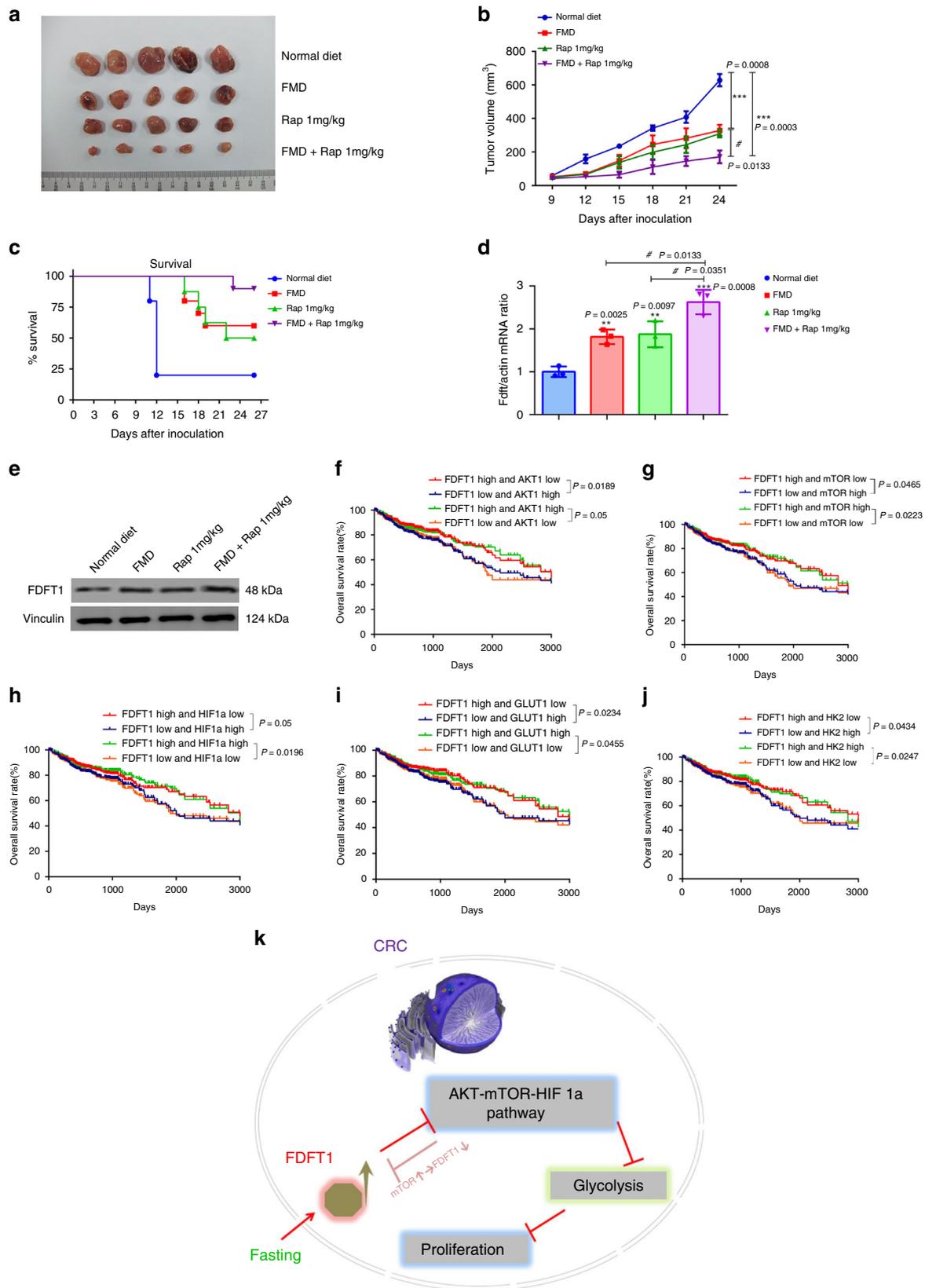
Proteomics. After samples were lysed in 1 \times protease inhibitor cocktail (Roche Ltd., Switzerland), the protein was digested with sequence-grade modified trypsin (Promega, WI) and lyophilized. The resultant peptide mixture was labeled with an iTRAQ 8-plex labeling kit (Sciex) following the manufacturer's instructions. The peptide mixture was fractionated by high pH separation using an Ultimate 3000 system (ThermoFisher Scientific, USA). The peptides were analyzed by on-line nanospray LC-MS/MS. Tandem mass spectra were processed by PEAKS Studio version 8.5 (Bioinformatics Solutions Inc., Canada). Differentially expressed proteins were filtered if their fold change was greater than 1.5 and they contained at least two unique peptides with a significance greater than 13. The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the data set identifier PXD012029 and 10.6019/PXD012029.

Clinical samples. CRC and paired noncancerous tissues were obtained from 81 patients who underwent surgical resection without preoperative chemotherapy or radiotherapy at FUSCC from 2012 to 2013. Prior patient consent and approval from the Institutional Research Ethics Committee were obtained. The patients were followed up after surgery every 3 months. All tissues were frozen at -125°C until use.

IHC staining. IHC staining of paraffin-embedded tissues with antibodies against *FDFT1* (Abcam, ab195046) was performed and scored according to standard procedures. The staining score was determined by two independent pathologists at our center.

Animal model. BALB/c mice (female, 4–6 weeks of age, 18–20 g; Shanghai SLAC Laboratory Animal Co., Ltd) were housed in a specific pathogen-free (SPF) environment. In total, 2×10^4 cells (CT26, CT26 pcDNA-*FDFT1*, or CT26 sh*FDFT1*) were injected subcutaneously into the right flank of the mice. When the tumors were palpable, the mice were randomly assigned to the control group or the FMD group. In the control group, food was provided ad libitum with TD.7912 rodent chow. The average daily consumption of mice was 14.9 kJ in the control group. The FMD consisted of three components^{11,67–70}, designated as the day 1 diet, day 2–3 diet, and day 4–7 diet, fed in this order. The day 1 diet contained only 50% of the calories of the normal intake, which consists of a variety of vegetable powders, low-calorie broth powders, essential fatty acids, extra virgin olive oil, minerals, and vitamins, containing 7.67 kJ/g; carbohydrate 2.2k J/g, protein 0.46k J/g, fat 5.00 kJ/g. The day 2–3 diet contained only 10% of the normal calories intake, which consists of glycerol and low-calorie broth powders, containing 1.48 kJ/g, carbohydrates 1.47 kJ/g, and protein/fat 0.01 kJ/g. For the day 4–7 diet, the mice were fed their normal intake; this progression was followed by another cycle of the FMD. The animals had free access to water. At the end of the study, the mice underwent microPET/CT scanning. After scanning, the tumors were surgically dissected. Fasting mimic group + glucose group were provided with 10 mg/kg glucose supplementation in the drinking water during the FMD. All animal experiments were performed according to the procedures approved by the Institutional Animal Care and Use Committee of Fudan University.

MicroPET/CT imaging. MicroPET/CT scanning and image analysis were performed using an Inveon microPET/CT system and the manufacturer-supplied display software (Inveon Research Workplace, Siemens Medical Solutions, USA). Each tumor-bearing mouse was injected with 5.55 MBq (150 μ Ci) of ^{18}F -fluorodeoxyglucose (^{18}F -FDG) via the tail vein. Ten-min static scans were acquired at 1.0 h post injection, and the animals were maintained under isoflurane anesthesia during the scanning period. The images were reconstructed using a three-



dimensional ordered-subset expectation-maximization (OSEM3D)/maximum algorithm. Inveon Research Workplace was used to obtain the maximum standard uptake value (SUVmax).

In vivo rapamycin treatment. Rapamycin (1 mg/kg/d, CAS 53123-88-9, Santa Cruz Biotechnology, USA) was injected into mice intraperitoneally when the tumors were palpable. FMD also was started when the tumors were palpable.

Total cholesterol levels. The total cell cholesterol levels were measured by a cholesterol/cholesteryl ester quantitation kit (Abcam, ab65359) according to the manufacturers' instructions.

Statistical analysis. The experiments were repeated at least three times. All data are presented as the means ± SDs. SPSS 17.0 software (IBM, USA) and GraphPad Prism 7.0 software were used for data analysis. Two-sided unpaired Student's *t*

Fig. 7 Fasting and mTOR inhibitor synergize in suppressing CRC proliferation and clinical significance of the FDFT1/AKT-mTOR-HIF1 α pathway in CRC patients. **a** CT26 cells were injected into BALB/c mice. When the tumors were palpable, the mice were randomly assigned to the normal diet group, FMD group, the rapamycin 1 mg/kg group and FMD + rapamycin 1 mg/kg group. Photograph of dissected tumors (the first line: normal diet, the second line: FMD, the third line: rapamycin 1 mg/kg, the fourth line: FMD + rapamycin 1 mg/kg, $n = 5$). **b** The tumor volumes were measured every 3 days after the 9th day ($n = 30$; $***P = 0.0008$, $P = 0.0003$; $\#P = 0.0133$). On day 9 after inoculation, all the tumor were palpable. **c** Kaplan–Meier analysis of the overall survival of mice after the inoculation in normal diet group, FMD group, normal diet mice treated with rapamycin 1 mg/kg group and FMD + rapamycin 1 mg/kg group ($n = 30$; log-rank score: $P = 0.0049$ for FMD group, $P = 0.0058$ for rapamycin 1 mg/kg group; $P = 0.00069$ for FMD + rapamycin 1 mg/kg group.) **d, e** The expression level of *FDFT1* in four groups was evaluated by western blotting and qRT-PCR ($**P = 0.0025$, $P = 0.0097$; $***P = 0.0008$; $\#P = 0.0133$, $P = 0.0351$). **f–j** Survival analysis stratified by combining *FDFT1* levels with *AKT1*, *mTOR*, *HIF1 α* , *GLUT1*, and *HK2* levels from CRC patients in the TCGA cohort. **k** Proposed model of the mechanism underlying the fasting-mediated regulation of glucose metabolism via the *FDFT1/AKT-mTOR-HIF1 α* axis in colorectal cancer. Fasting upregulates the expression of *FDFT1* during the inhibition of colorectal cancer cell aerobic glycolysis and proliferation. *FDFT1*, whose downregulation is correlated with malignant progression and poor prognosis in CRC, acts as a critical tumor suppressor in CRC. We then observed that *FDFT1* is an important downstream target of fasting that mediates the inhibition of CRC cell proliferation. Mechanistically, *FDFT1* inhibits the *AKT-mTOR-HIF1 α* pathway, impairing aerobic glycolysis, and thereby suppressing the proliferation of CRC cells. There is also a reverse regulation of *FDFT1* by *mTOR*. Error bars, mean \pm SD, the data are from three independent experiments. Two-sided t tests. Kaplan–Meier analysis and log-rank tests were used in panel **c**. $*P < 0.05$, $**P < 0.01$, $***P < 0.001$, compared with normal diet group. $\#P < 0.05$, $\#\#P < 0.01$.

tests, one-way analysis of variance, chi-square tests, Kaplan–Meier analysis and log-rank tests were used to evaluate the data. Differences were considered significant at $*P < 0.05$; $**P < 0.01$; $***P < 0.001$; $****P < 0.0001$; $\#P < 0.05$; and $\#\#P < 0.01$.

Reporting summary. Further information on research design is available in the Nature Research Reporting Summary linked to this article.

Data availability

Raw mass spectrometry proteomics data files have been deposited in the ProteomeXchange Consortium with the data set identifier PXD012029 and 10.6019/PXD012029. All the other data supporting the findings of this study are available within the article and its supplementary information files and from the corresponding author upon reasonable request. A reporting summary for this article is available as a Supplementary Information file.

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Author contributions

M.L.W., D.M., and C.H.M. designed the study; M.L.W., X.Y.C., H.L., Z.R.S., M.M.Z., and P.F.S. performed the experiments; Q.Y., Y.J.X., and N.J. analyzed the data; J.P.Z. and J.Z. provided reagents; M.L.W. and W.K.C. wrote the paper; M.L.W. and X.P.Z. revised the paper.

Competing interests

The authors declare no competing financial interests.

Additional information

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